

Amendments to the Specification:

Please replace the paragraph beginning at page 21, line 24, with the following rewritten paragraph:

Human genomic factor V Leiden DNA sequence: Primer: 5"-ACA AAA TAC CTG TAT TCC TT-3- (SEQ ID NO : 11), wild type template : 5-GAT CCC TGG ACA GGC GAG GAA TAC AGG TAT TTT GT-3 (SEQ ID NO :12_30), mutant template: 5'- GAT CCC TGG ACA GGC AAG GAA TAC AGG TAT TTT GT-3' (SEQ ID NO :12_31).

Please replace the paragraph beginning at page 21, line 29 with the following rewritten paragraph:

Human somatic BRAF-T1796A mutation: Primer: 5-GAC CCA CTC CAT CGA GAT TTC T-3' (SEQ ID NO : 13), wild type template : 5-GGT CTA GCT ACA GTG AAA TCT CGA TGG AGT GGG TC-3' (SEQ ID NO :14_32), mutant template : 5-GGT CTA GCT ACA GAG AAA TCT CGA TGG AGT GGG TC-3' (SEQ ID NO :14_33).

Please replace the paragraph beginning at page 22, line 1, with the following rewritten paragraph:

Human dihydropyrimidine dehydrogenase (DpyD) mutation G735A : Primer : 5-GTT TTA GAT GTT AAA TCA CAC TTA T-3' (SEQ ID NO : 15), wild type template : 5'-CTT TCC AGA CAA CGT AAG TGT GAT TTA ACA TCT AAA AC-3' (SEQ ID NO :1634), mutant template : 5'-CTT TCC AGA CAA CAT AAG TGT GAT TTA ACA TCT AAA AC- 3' (SEQ ID NO :1635).

Please replace the paragraph beginning at page 22, line 7, with the following rewritten paragraph:

Human acid ceramidase mutation A107G: Primer : 5'-CGT TGG TCC TGA AGG AGG AT-3' (SEQ ID NO : 17), wild type template : 5'-AAA TCA ACC TAT CCT CCT TCA

GGA CCA ACG TAC-3 (SEQ ID NO : 1836), mutant template : 5'-AAA TCA ACC TGT CCT CCT TCA GGA CCA ACG TAC-3' (SEQ ID NO : 1837).

Please replace the paragraph beginning at page 25, line 1, with the following rewritten paragraph:

With the two mutants mentioned, primer extension assays according to Example 3 were performed. The mismatch discrimination with the human genomic factor V Leiden DNA sequence was tested: Primer: 5'-ACA AAA TAC CTG TAT TCC TT-3' (SEQ ID NO: 11), wild type template: 5'-GAT CCC TGG ACA GGC GAG GAA TAC AGG TAT TTT GT-3' (SEQ ID NO: 1230), mutant template: 5'-GAT CCC TGG ACA GGC AAG GAA TAC AGG TAT TTT GT-3' (SEQ ID NO: 1231). The tendencies of the two mutants to extend mismatches as compared to canonic complexes were compared. As shown in Figure 5, the QVA mutant has a substantially higher tendency to extend mismatches as compared to the LVL mutant.

Please delete the section of the application entitled "Sequence Listing" immediately after the Abstract on page 30 and insert the enclosed Sequence Listing therefor.